

#8
6403

10001

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,414A

DATE: 01/23/2003

TIME: 08:07:07

Input Set : A:\6280M.txt

Output Set: N:\CRF4\01232003\I869414A.raw

4 <110> APPLICANT: Gurney et al.

6 <120> TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
USES

7 THEREFOR

9 <130> FILE REFERENCE: 28341/6280M

C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/869,414A

C--> 12 <141> CURRENT FILING DATE: 2001-06-27

14 <150> PRIOR APPLICATION NUMBER: 09/416,901

15 <151> PRIOR FILING DATE: 1999-10-13

17 <150> PRIOR APPLICATION NUMBER: 60/155,493

18 <151> PRIOR FILING DATE: 1999-09-23

20 <150> PRIOR APPLICATION NUMBER: 09/404,133

21 <151> PRIOR FILING DATE: 1999-09-23

23 <150> PRIOR APPLICATION NUMBER: PCT/US99/20881

24 <151> PRIOR FILING DATE: 1999-09-23

26 <150> PRIOR APPLICATION NUMBER: 60/101,594

27 <151> PRIOR FILING DATE: 1998-09-24

29 <160> NUMBER OF SEQ ID NOS: 74

31 <170> SOFTWARE: PatentIn Ver. 2.0

33 <210> SEQ ID NO: 1

34 <211> LENGTH: 1804

35 <212> TYPE: DNA

36 <213> ORGANISM: Homo sapiens

38 <400> SEQUENCE: 1

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40 gccccggagc tggcccccgc gcccttcacg ctgccctcc ggggtggccgc ggccacgaac 120

41 cgcgtagttg cgcccacccc gggaccggg acccctgccg agcgccacgc cgacggcttg 180

42 gcgctcgccc tggagcctgc cctggcgctc ccgcggggcg ccgccaactt cttggccatg 240

43 gtagacaacc tgcaggggga ctctggccgc ggctactacc tggagatgct gatcgggacc 300

44 cccccgcaga agctacagat tctcgttgac actggaagca gtaactttgc cgtggcagga 360

45 accccgcact cctacataga cacgtacttt gacacagaga ggtctagcac ataccgctcc 420

46 aagggctttg acgtcacagt gaagtacaca caagggaagct ggacgggctt cgttggggaa 480

47 gacctcgtea ccatccccaagggttcaat acttcttttc ttgtcaacat tgccactatt 540

48 tttgaatcag agaatttctt ttgacctggg attaaatgga atggaatact tggcctagct 600

49 tatgccacac ttgccaagcc atcaagttct ctggagacct tcttcgactc cctggtgaca 660

50 caagcaaaca tccccaacgt tttctccatg cagatgtgtg gagccggctt gcccggttgc 720

51 ggatctggga ccaacggagg tagtcttgct ttgggtggaa ttgaaccaag tttgtataaa 780

52 ggagacatct ggtatacccc tattaaggaa gagtggtagt accagataga aattctgaaa 840

53 ttggaaattg gaggccaaag ccttaatctg gactgcagag agtataacgc agacaaggcc 900

54 atcgtggaca gtggcaccac gctgctgcgc ctgcccaga aggtgtttga tgcggtggtg 960

55 gaagctgtgg ccgcgcac tctgattcca gaattctctg atggtttctg gactgggtcc 1020

56 cagctgtgcg gctggacgaa ttgcgaaaca ccttggtctt acttccctaa aatctccatc 1080

57 tacctgagag atgagaactc cagcaggtca ttccgtatca caatcctgcc tcagctttac 1140

58 attcagccca tgatgggggc cggcctgaat tatgaatggt accgattcgg catttcccca 1200

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59 tccacaaatg cgctggtgat cggtgccacg gtgatggagg gcttctacgt catcttcgac 1260
60 agagcccaga agaggggtggg cttcgcagcg agcccctgtg cagaaattgc aggtgctgca 1320
61 gtgtctgaaa tttccggggcc tttctcaaca gaggatgtag ccagcaactg tgtccccgct 1380
62 cagtctttga gcgagcccat tttgtggatt gtgtcctatg cgctcatgag cgtctgtgga 1440
63 gccatcctcc ttgtcttaat cgtcctgctg ctgctgccgt tccggtgtca gcgtcgcccc 1500
64 cgtgaccctg aggtcgtaaa tgatgagtc tctctggtca gacatcgctg gaaatgaata 1560
65 gccaggcctg acctcaagca accatgaact cagctattaa gaaaatcaca tttccagggc 1620
66 agcagccggg atcgatggtg gcgctttctc ctgtgccac ccgtcttcaa tctctgttct 1680
67 gctcccagat gccttctaga ttcactgtct tttgattctt gattttcaag ctttcaaatc 1740
68 ctccctactt ccaagaaaaa taattaaaaa aaaaacttca ttctaaacca aaaaaaaaaa 1800
69 aaaa 1804

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71 <210> SEQ ID NO: 2

72 <211> LENGTH: 518

73 <212> TYPE: PRT

74 <213> ORGANISM: Homo sapiens

76 <400> SEQUENCE: 2

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80 Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
81           20           25           30
83 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
84           35           40           45
86 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
87           50           55           60
89 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
90   65           70           75           80
92 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
93           85           90           95
95 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
96           100          105          110
98 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
99           115          120          125
101 Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
102           130          135          140
104 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
105 145          150          155          160
107 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
108           165          170          175
111 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
112           180          185          190
114 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
115           195          200          205
117 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
118           210          215          220
120 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
121 225          230          235          240
123 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
124           245          250          255
127 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp

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Input Set : A:\6280M.txt

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128          260          265          270
130 Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
131          275          280          285
133 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
134          290          295          300
136 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
137 305          310          315          320
139 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
140          325          330          335
142 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
143          340          345          350
145 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
146          355          360          365
148 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
149          370          375          380
151 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
152 385          390          395          400
154 Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
155          405          410          415
157 Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
158          420          425          430
160 Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
161          435          440          445
163 Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
164          450          455          460
167 Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
168 465          470          475          480
170 Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg Cys
171          485          490          495
173 Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
174          500          505          510
176 Val Arg His Arg Trp Lys
177          515

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180 <210> SEQ ID NO: 3

181 <211> LENGTH: 2070

182 <212> TYPE: DNA

183 <213> ORGANISM: Homo sapiens

185 <400> SEQUENCE: 3

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187 ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcg cccctgggg 120
188 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
189 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
190 gtgggcagcc cccgcgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
191 gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360
192 taccgggacc tccggaagg tgtgtatgtg ccctacaccc agggcaagt ggaaggggag 420
193 ctggggaccg acctggttaag catccccat ggccccaacg tcaactgtgc tgccaacatt 480
194 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattcctg 540
195 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
196 ctggtaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660

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Input Set : A:\6280M.txt

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197 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 720
198 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcgga gtggtattat 780
199 gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
200 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
201 gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
202 ggtttctggc taggagagca gctgggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
203 ttcccagtca tctcactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1080
204 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
205 tacaagtttg ccatctcaca gtcatccacg ggcactgtta tgggagctgt tatcatggag 1200
206 ggcttctacg ttgtctttga tcgggcccga aaacgaattg gctttgctgt cagcgcttgc 1260
207 catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320
208 gaagactgtg gctacaacat tccacagaca gatgagtcaa ccctcatgac catagcctat 1380
209 gtcatggctg ccatctgcgc cctcttcatg ctgccactct gcctcatggt gtgtcagttg 1440
210 cgctgcctcc gctgcctgcg ccagcagcat gatgactttg ctgatgacat ctccctgctg 1500
211 aagtgaggag gcccatgggc agaagataga gattcccctg gaccacacct ccgtggttca 1560
212 ctttggtcac aagtaggaga cacagatggc acctgtggcc agagcacctc aggacctcc 1620
213 ccaccaccca aatgcctctg ccttgatgga gaaggaaaag gctggcaagg tgggttccag 1680
214 ggactgtacc ttaggaaac agaaaagaga agaaaagagc actctgctgg cgggaatact 1740
215 cttggtcacc tcaaatttaa gtcgggaaat tctgtgctt gaaacttcag ccctgaacct 1800
216 ttgtccacca ttcttttaa ttctccaacc caaagtattc ttcttttctt agtttcagaa 1860
217 gtactggcat cacacgcagg ttaccttggc gtgtgtccct gtggtaccct ggcagagaag 1920
218 agaccaagct tgtttccctg ctggccaaag tcagtaggag aggatgcaca gtttgctatt 1980
219 tgcttttagag acagggactg tataaacaag cctaacattg gtgcaaagat tgcctcttga 2040
220 attaaaaaaaa aaaaaaaaaa aaaaaaaaaa
221                                     2070

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222 <210> SEQ ID NO: 4

223 <211> LENGTH: 501

224 <212> TYPE: PRT

225 <213> ORGANISM: Homo sapiens

227 <400> SEQUENCE: 4

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231 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
232           20           25           30
234 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
235           35           40           45
237 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
238           50           55           60
240 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
241   65           70           75           80
243 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
244           85           90           95
246 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
247           100          105          110
250 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
251           115          120          125
254 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
255           130          135          140
257 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
258 145          150          155          160

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260 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
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263 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
264          180          185          190
266 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
267          195          200          205
269 Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
270          210          215          220
272 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
273 225          230          235          240
275 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
276          245          250          255
278 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
279          260          265          270
281 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
282          275          280          285
284 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
285          290          295          300
287 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
288 305          310          315          320
290 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
291          325          330          335
293 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
294          340          345          350
296 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
297          355          360          365
299 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
300          370          375          380
302 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
303 385          390          395          400
305 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
306          405          410          415
308 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
309          420          425          430
312 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
313          435          440          445
315 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
316          450          455          460
318 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
319 465          470          475          480
321 Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
322          485          490          495
324 Ile Ser Leu Leu Lys
325          500
328 <210> SEQ ID NO: 5
329 <211> LENGTH: 1977
330 <212> TYPE: DNA
331 <213> ORGANISM: Homo sapiens
333 <400> SEQUENCE: 5

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/23/2003
PATENT APPLICATION: US/09/869,414A TIME: 08:07:08

Input Set : A:\6280M.txt
Output Set: N:\CRF4\01232003\I869414A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:74; Xaa Pos. 1,2,3,4

VERIFICATION SUMMARY

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Input Set : A:\6280M.txt

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:3890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0